

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.0465 Seconds
(without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613B-6

Perfect score: 583
Sequence: 1 MDMLTFQKKHLNTRDVC.....TFCVTCENQAPVHFVGVC 105

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	94.9	104	2 A39035	ribonuclease-relat
2	289	49.6	111	2 A27121	ribonuclease-relat
3	285.5	49.0	111	1 JX0120	ribonuclease-relat
4	269.5	46.2	111	2 JX0085	pancreatic ribonuc
5	149	25.6	119	2 S41111	pancreatic ribonuc
6	131	22.5	124	1 NR01	pancreatic ribonuc
7	128	22.0	125	1 A32474	angiogenin [valida
8	126	21.6	128	1 NRCU	pancreatic ribonuc
9	125	21.4	124	1 NRMK	pancreatic ribonuc
10	120	20.6	128	1 NRKS	pancreatic ribonuc
11	119.5	20.5	145	1 A35932	angiogenin precurs
12	119	20.4	128	1 NRCP	pancreatic ribonuc
13	117	20.1	124	1 NRFB	pancreatic ribonuc
14	116	19.9	125	1 B43825	angiogenin - rabbi
15	116	19.9	128	1 NRY	pancreatic ribonuc
16	114	19.6	124	1 NRHP	pancreatic ribonuc
17	113	19.4	147	1 NRHAG	angiogenin precurs
18	112	19.2	124	1 NRBO	pancreatic ribonuc
19	112	19.2	124	1 NRBO	pancreatic ribonuc
20	112	19.2	124	2 JCS560	pancreatic ribonuc
21	112	19.2	150	1 NRBO	pancreatic ribonuc
22	111.5	19.1	147	2 TS2489	pancreatic ribonuc
23	111	19.0	124	2 NRHO	pancreatic ribonuc
24	111	19.0	128	1 NRHO	pancreatic ribonuc
25	111	19.0	128	1 NRPO	pancreatic ribonuc
26	111	19.0	167	2 S20066	pancreatic-type ri
27	110.5	19.0	123	1 A43825	angiogenin - pig
28	110.5	19.0	155	2 JC6159	eosinophil-associa
29	109	18.7	124	1 NRSH	pancreatic ribonuc

30	109	18.7	124	1 NRPRH	pancreatic ribonuc
31	109	18.7	124	1 NRCPA	pancreatic ribonuc
32	109	18.7	124	2 S07141	pancreatic ribonuc
33	108	18.5	124	1 NRMB	pancreatic ribonuc
34	108	18.5	124	1 NRGN	pancreatic ribonuc
35	107	18.4	124	1 NRGF	pancreatic ribonuc
36	106	18.2	156	2 JC6160	eosinophil-associa
37	105	18.0	124	1 NRDEO	pancreatic ribonuc
38	105	18.0	124	1 NRCM	pancreatic ribonuc
39	105	18.0	124	1 NRCM	pancreatic ribonuc
40	105	18.0	124	1 NRCMB	pancreatic ribonuc
41	105	18.0	128	1 NRCW2	pancreatic ribonuc
42	104	17.8	124	1 NRYH	pancreatic ribonuc
43	103	17.7	124	1 NRDER	pancreatic ribonuc
44	103	17.7	124	1 NRDEN	pancreatic ribonuc
45	103	17.7	124	1 NREKN	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W., Mikulski, S.M., Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 94.9%; Score 553; DB 2; Length 104;

Best Local Similarity 95.2%; Pred. No. 1,1e-48;

Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY	2	QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLT 61
DB	1	EDMLTFQKKHITNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPKAICKGIASKNVLT 60
QY	62	SEFYLSDCNVTSRCKYKLRKSTNTFCVTCENQAPVHFVGVC 105
DB	61	SEFYLSDCNVTSRCKYKLRKSTNTFCVTCENQAPVHFVGVC 104

RESULT 2

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K., Takio, K., Kuwada, M., Nitta, K., Sakakibara, F., Kawachi, H., Takayan

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeian

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RTT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 49.6%; Score 289; DB 2; Length 111;

Best Local Similarity 48.6%; Pred. No. 4,4e-22;

Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY	2	QDWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNFTYSRPEPKAICKGIASKN 57
DB	1	ENMATEFOKKHIIINPIINCMTIMDNITIVIGCOCKRVNFTISSATTVKATGVI-NMN 59

```
OY      58 VLTSTSEFYISDC---NVTSRPCKKYLKKSTMTFCVTCENQAPVHFGVGHC   105
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      60 VLSTRFQLNTCTRTSITPRPCPYSSRTEYNICVKCENQYPVHFGAGIGRC   110
```

RESULT 3

ribonuclease-related sialic acid-binding lectin - Japanese frog
C.Species: Rana japonica (Japanese frog)
C.Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999
C.Accession: JX0120
R.Kamiya, Y.; Oyama, F.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi, R.
J. Biochem. 108, 139-143, 1990
A.Title: Amino acid sequence of a lectin from Japanese frog (*Rana japonica*) eggs.
A.Reference number: JX0120; MUID:9105319; PMID:2228005

Query Match	49.0%	Score 285.5	DB 1	Length 111
Best Local Similarity	45.0%	Pred. No. 9.8e-22		
Matches	50	Conservative 19	Mismatches 35	Indels 7
				Gaps 2

QY 2 QDWLTFQKKHLNTRDYDCNNMTSTNLE----HCKDKNTFIYSRREPVAKICGIIATSKN 577

Db 1 QNMAKFEKHLNPTNSINCNTLMDKSIYIVGGCKERNFTIISSATVYKALCSGASTNRN 600

```
QY      58 VLTITSEFYLSDC---NTTSRPCKKYLKKSTNFTCVTCENQAPHPFVGVGHC 105
          ||::| | : |   || | : || |::||| | : |
Db      61 VLSTTRQLNTCIRSATAPRCPYNSTRETNVICVKCENTRLPYPHFAIGIRC 111
```

RESULT 4

C:Pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C:Date: 07-Sep-1990 #sequence-revision 07-Sep-1990 #text-change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katsuyama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ong
 J. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <NIT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; pyroglutamic acid
 E:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10.35.104/Active site: His, Lys, His #status predicted
 F:19-72.34-82.52-97.94-111/Disulfide bonds: #status predicted

Query Match	46.2%	Score 269.5	DB 2	Length 11
Best Local Similarity	43.2%	Pred. No. 4e-20		
Matches 48	Conservative 19	Mismatches 37	Indels 7	Gaps 2

QY 2 QDWLTFQKKHLNTRDYDCNNIMSTNLE----HCKDKNFIYSRREPVAICIGLIASKN 57

Db 1 QNMAKFEKEKHIRSTSSIDCNIIMDKAIYIVGCKEKERNFIISSEDNVKAICSGVSPDRK 60

```

Qy      58 VLTITSEYLSDC---NVTSRPCKKLLKSTNFCVTCENQAPRHVGVGHC 105
          | : | : | : | : | : | : | : | : | : | : | : | : |
Db      61 ELSTYSFKLNTCIRDSITPRPCPYHPSPDNKKICVKCEKQLPVHFGVIGCK 111

```

RESULT 5

S41111
pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S41111
R:Zhao, W., Beintema, J.J.: Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of Iguana (Iguana iguana) pancreatic ribonuclease
#:Reference number: S41111; MUID:94139745; PMID:8307028

Query Match	25.6%	Score 149;	DB 2;	Length 119;
Best Local Similarity	30.7%	Pred. No. 5.7e-08;		
Matches 35;	Conservative 19;	Mismatches 44;	Indels 16;	Gaps 5.

Oy 2. QDWLTFQKKHL-----TNTKRVDCNNIM---STNLFHCKDKDNFTIYSREPVKALIC--k 50
|||::|||::: |: | : ||: ||::: | :::
Db 1 QDWSFQNKHIDYPTETASNPAYCCLMGRNLINPFCCTRNTEVFHASSEIQVCGSG 60

QY 51 GIASKNVLTSE-FYLSDC----NVTSRCKKYLKKSTNTFCVTCENQAPVHF 99
| : :: | : || | : ||| ||||
Db 61 GHYYEDNLDSNESFDLTDCKNVGTA PSSCKYNGIPGTKRIRACENNQPVHF 114

RESULT 6

pancreatic ribonuclease (EC 3.1.27.5) - cufs
 N/Alternate names: RNase 1; RNase A
 C/Species: *Galea musteloides* (cufs)
 C/Date: 03-Aug-1994 #sequence_revision 03-Aug-1994 #text_change 04-Oct-1996
 C/Accession: A00837
 R/Reintema, J.J.; Neutboom, B.
 J Mol. Evol. 19, 145-152, 1983
 A/Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the
 reference numbers: A92937; MUID:87036770; PMID:5371215

Query Match	22.5%	Score	131	DB 1	Length	124			
Best Local Similarity	30.6%	Pred. No.	3	8e-06					
Matches	37	Conservative	18	Mismatches	34	Indels	32	Gaps	7

Dy 5 LTFQKKHL-----TNTROVDCCNNIM--STNLFHCXDKNTFTYSRPEVKALCKGILA 54
 : |||: | | | | | | | | | |
 Dd 6 MKFQRFQMDSGDGHPRDTNTN--YCNEKMWVRSMTQGRCKPVNTFEHRLPLAQAQC----S 59

QY 55 SKNV-----LTTSEFLSDCNVTSNP---CKYLLKSTNFCVTCEN--QAPVH 98
 ||| :| :||| ||| |::: :| ||| |||
 Db 60 QKVPCKNGQNCYQSHSSMRITDCRVTSSSKYPMCSYRMTQQAQSLIVACEGTPSPVH 119

QY	99 F 99
Db	120 F 120

RESULT 7

angiogenin [validated] - bovine
 N:Alternate names: angiogenesis factor
 N:Contains: ribonuclease (EC 3.1.27.-)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
 /Accession: A32474; S02001; A30044; S48212

R:Bond, M.D.: Strydom, D.J.
 Biochemistry 28, 6110-6113, 1989
 A:Title: Amino acid sequence of bovine angiotensin.
 A:Reference number: A32474; MUID:89375344; PMID:2775757
 A:Accession: A32474
 A:Molecule type: protein
 A:Residues: 1-125 <BON>
 A:Experimental source: Plasma
 R:Meis, P.; Damatt, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
 FEBS Lett. 241, 41-45, 1988
 A:Title: The complete amino acid sequence of bovine milk angiotensin.
 A:Reference number: S02001; MUID:89065101; PMID:3197858
 A:Accession: S02001
 A:Molecule type: protein
 A:Residues: 1-125 <MAE>
 A:Experimental source: milk
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 submitted to the Brookhaven Protein Data Bank, January 1995
 A:Reference number: A65065; PDB:1AG1
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
 A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
 A:Reference number: A58315; MUID:95224037; PMID:7708754
 A:Contents: annotation: X-ray crystallography, 1.5 angstroms
 R:Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 submitted to the Brookhaven Protein Data Bank, April 1996
 A:Accession: A65709; PDB:1G10
 A:Contents: annotation: conformation by (1)H-NMR, residues 1-125
 R:Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
 Biochemistry 35, 8870-8880, 1996
 A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spec
 A:Reference number: A58821; MUID:96280645; PMID:8688423
 A:Contents: annotation: conformation by (1)H-NMR
 R:Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
 Eur. J. Biochem. 224, 811-822, 1994
 A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.
 A:Reference number: S48212; MUID:95010071; PMID:7925406
 A:Contents: annotation: conformation by (1)H-NMR
 C:Function:
 A:Description: hydrolyzes tRNA, induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiotensin; hydrolase; nucleic acid degradation
 F:60-68/Region: receptor binding #status predicted
 F:14,115/Active site: His, Lys, His #status predicted
 F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 22.0%; Score 128; DB 1; Length 125;
 Best Local Similarity 34.0%; Pred. No. 7.7e-06;
 Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

OY 17 DVDCNNMSTNLF--HCKDKNTFLYSRPEPVKAICKIISKN-----VLTTSFYL 66
 DB 24 DEYCFNMKRRRLTRPCKDKRNTFLHGKNDKAIACE---DRGQPYRGDLRIKSKSEFQI 79

OY 67 SDC---NVTSR-PCKYKLKSTNFCVTCENQAPVHF 99
 DB 80 TCKHKGGSSRPCRGATGDSRIYVGCENGLPVHF 116

RESULT 8
 NRCU
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C:Date: 24-Apr-1984 #sequence-revision 30-Sep-1988 #text-change 31-Mar-2000
 C:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
 A:Reference number: A90612; MUID:77065676; PMID:999896
 A:Accession: A00822
 A:Molecule type: protein

A:Residues: 1-128 <VAN>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.6%; Score 126; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 1.3e-05;
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

OY 7 FOKKHL-----TTRVDCCNNIN-STNLF--HCKDKNTFLYSRPEPVKAICKIISKNV 58
 DB 8 FERQHDNRSGSPSTNPNYCNEMKSRNMOGRCKPVNTFVEHPLADVOAHC---FOKNV 63

OY 59 L-----TTSFYLSDCNVTSRP---CKYKLKSTNFCVTCENQ--APVHF 99
 DB 64 LCRNGOTNCYOSNMHITDCRYTNSDYPNCYSRTSQEBSIVACEGNPVVPHF 120

RESULT 9
 NRMK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale
 N:Alternate names: RNase 1; RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C:Date: 24-Apr-1984 #sequence-revision 24-Apr-1984 #text-change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Welling, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.4%; Score 125; DB 1; Length 124;
 Best Local Similarity 28.6%; Pred. No. 1.5e-05;
 Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 5 LTFOKKHLTTRVD-----CNNIMSTNLF--HCKDKNTFLYSRPEPVKAICKIISK 56
 DB 6 MKFQRHMDSGNSPNNPNYCNOMMKRRKKTQGRCKRVNFFHESLEDAVAVC---SKR 61

OY 57 NVL-----TTSFYLSDCNVTSRP---CKYKLKSTNFCVTCENQ--APVHF 99
 DB 62 NVLCKNGRTNCYESNSTMHTTDCRQGGSSKYPNCAVKTQSKERKHIIVACGNGPVVPHF 120

RESULT 10
 NRKS
 pancreatic ribonuclease (EC 3.1.27.5) - casiragua
 C:Species: Proechimys guairae (casiragua)
 C:Date: 17-Mar-1987 #sequence-revision 17-Mar-1987 #text-change 30-Sep-1993
 C:Accession: A00821
 R:Beintema, J.J.; Knol, G.; Martena, B.
 Biochim. Biophys. Acta 705, 102-110, 1982
 A:Title: The primary structures of pancreatic ribonucleases from African porcupine an
 A:Reference number: A90644; MUID:83000399; PMID:7115727
 A:Accession: A00821
 A:Molecule type: protein
 A:Residues: 1-128 <BEI>
 A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

F:21,34/Binding site: carbohydrate (asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match          20.4%: Score 119; DB 1; Length 128;
Best Local Similarity 26.9%: Pred. No. 6,4e-05;
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;

QY 5 LTRQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPYAICGIIAS 55
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00820
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
F:36-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match          20.1%: Score 117; DB 1; Length 124;
Best Local Similarity 26.9%: Pred. No. 9,8e-05;
Matches 32; Conservative 19; Mismatches 40; Indels 28; Gaps 6;

QY 5 LTRQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPYAICGIIAS 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 MKFQROHMDEGSSPSSTNANYCNEMKGRNMTQGYCKPVNFVHEPLADYAVC---FQK 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 NV-----LTTSEFLSDCNVTSRP---CKTKLKSTNTFCVTCENQ--APVHF 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 NVFCCKKNGQSNCYOSNSNMHTTDCRLTNSKRYPMCSYRTSRKNGIIVACEGPNYPVHF 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
angiogenin - rabbit
B43825
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29833; B43825
R:Bond, M.D.; Striydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discer
A:Reference number: S29833; PMID:93192291; PMID:8448182
A:Accession: S29833
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-125 <RON>
A:Note: submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match          19.9%: Score 116; DB 1; Length 125;
Best Local Similarity 31.2%: Pred. No. 0.00012;
Matches 24; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

```

Qy 31 KCKNEPTYSRPEPVKICK---GIASKV-LTTESEFLSDCNVTS---PRCKRLK 82
 ||| ||| : : : : : ||| : : : : : ||| :
 Db 39 CKDPTFVHONKSGIKVCEEDKNGKPFYKNFRISKSPQYITCKHVGSGPWPCRRANS 98
 : : : : : : : : : : : : : : : : : :
 Qy 83 STNFCYTCENQAPVHF 99
 : : : : : ||| |||
 Db 99 GSRNVIACENGCLPVHF 115

RESULT 15

pancreatic ribonuclease (EC 3.1.27.5) - capybara
N:Alternate names: RNase 1; RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A00824
R:Beintema, J.-J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amniotic and embryonic
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00824
A:Molecule type: protein
A:Residues: 1-128 <BEI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; nucleic acid digestion; pancreas
F:12-41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match	19.9%	Score 116:	DB 1:	Length 128;
Best Local Similarity	27.8%	Pred. No. 0.00013:		
Matches	32;	Conservative	21;	Mismatches 42;
			Indels	20;
			Gaps	6;

```
Oy 5 LTFQKHL-----TTFEDVCCNNIMSNPL--HCNDKNFEIYSRPEPKAIC-KIIILS 55
Dy 6 MKFGRQHVHDEGSSSSSSNANCENMVARRKNTDQRCKRPVNFVEHPEIADVAGVCFQKNCVC 65
Oy 56 KNVLT-----SEFYLSDCNVYTSR---PKYIKLKSTNFCYTCENQ--APHPF 99
Dy 66 KNGQTNCYQSYISNHIITDCRYATSKSRKPPDCTSYTTQAQKSIIVACBENLIVYHPHF 120
```

Search completed: June 25, 2003, 14:58:02
Job time : 13.0465 secs

